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STIC Biotechnology Systems Branch**RAW SEQUENCE LISTING**
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/590,457
Source: DET
Date Processed by STIC: 09/05/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENT/IN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chknote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service; Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/590,457

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence. (see item 11 below)
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use
 of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
 Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
 explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
 Sequence Rules
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

RAW SEQUENCE LISTING

DATE: 09/05/2006

PATENT APPLICATION: US/10/590,457

TIME: 15:11:48

Input Set : E:\Sequence Listing-13987-00020-US.txt

Output Set: E:\CRF4\09052006\J590457.rtf

3 <110> APPLICANT: Cirpus, Petra

4 Bauer, Jorg

5 Qiu, Xiao

6 Wu, Guohai

7 Datla, Nagamani

9 <120> TITLE OF INVENTION: METHOD FOR PRODUCING POLYUNSATURATED FATTY ACIDS IN

TRANSGENIC

10 PLANTS

12 <130> FILE REFERENCE: 13987-00020-US

C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/590,457

C--> 14 <141> CURRENT FILING DATE: 2006-08-25

14 <150> PRIOR APPLICATION NUMBER: PCT/EP2005/001863

15 <151> PRIOR FILING DATE: 2005-02-23

17 <150> PRIOR APPLICATION NUMBER: DE 10 2004 009 457.8

18 <151> PRIOR FILING DATE: 2004-02-27

20 <150> PRIOR APPLICATION NUMBER: DE 10 2004 012 370.5

21 <151> PRIOR FILING DATE: 2004-03-13

23 <150> PRIOR APPLICATION NUMBER: DE 10 2004 017 518.7

24 <151> PRIOR FILING DATE: 2004-04-08

26 <150> PRIOR APPLICATION NUMBER: DE 10 2004 024 014.0

27 <151> PRIOR FILING DATE: 2004-05-14

29 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/07957

30 <151> PRIOR FILING DATE: 2004-07-16

32 <150> PRIOR APPLICATION NUMBER: DE 10 2004 062 543.3

33 <151> PRIOR FILING DATE: 2004-12-24

35 <160> NUMBER OF SEQ ID NOS: 255

37 <170> SOFTWARE: PatentIn version 3.3

40 <210> SEQ ID NO: 1

41 <211> LENGTH: 1266

42 <212> TYPE: DNA

43 <213> ORGANISM: Euglena gracilis

45 <220> FEATURE:

46 <221> NAME/KEY: CDS

47 <222> LOCATION: (1)..(1266)

48 <223> OTHER INFORMATION: Delta-8 desaturase

50 <400> SEQUENCE: 1

51 atg aag tca aag cgc caa gcg ctt ccc ctt aca att gat gga aca aca 48

52 Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr

53 1 5 10 15

56 tat gat gtg tct gcc tgg gtc aat ttc cac cct ggt ggt gcg gaa att 96

57 Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile

58 20 25 30

60 ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg 144

61 Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met

CPS-7)
Does Not Comply
Corrected Diskette Needed

CPS-6)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/590,457

DATE: 09/05/2006

TIME: 15:11:48

Input Set : N:\Sequence Listing-13987-00020-US.txt

Output Set: N:\CRF4\09052006\J590457.raw

62	35	40	45	
64	cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat	192		
65	His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn			
66	50 55 60			
68	ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa got caa gag	240		
69	Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu			
70	65 70 75 80			
72	gat ttc cgg aag ctc cga gaa gag ttg atc gca act ggc atg ttt gat	288		
73	Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp			
74	85 90 95			
76	gcc tcc ccc ctc tgg tac tca tac aaa atc agc acc aca ctg ggc ott	336		
77	Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu			
78	100 105 110			
80	gga gtg ctg ggt tat ttc ctg atg gtt cag tat cag atg tat ttc att	384		
81	Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile			
82	115 120 125			
84	ggg gca gtg ttg ctt ggg atg cac tat caa cag atg ggc tgg ctt tct	432		
85	Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser			
86	130 135 140			
89	cat gac att tgc cac cac cag act ttc aag aac cgg aac tgg aac aac	480		
90	His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn			
91	145 150 155 160			
93	ctc gtg gga ctg gta ttt ggc aat ggt ctg caa ggt ttt tcc gtg aca	528		
94	Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr			
95	165 170 175			
97	tgc tgg aag gac aga cac aat gca cat cat tcg gca acc aat gtt caa	576		
98	Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln			
99	180 185 190			
101	ggg cac gac cct gat att gac aac ctc ccc ctc tta gcc tgg tct gag	624		
102	Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu			
103	195 200 205			
105	gat gac gtc aca cgg gcg tca ccg att tcc cgc aag ctc att cag ttc	672		
106	Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe			
107	210 215 220			
109	cag cag tat tat ttc ttg gtc atc tgt atc ttg ttg cgg ttc att tgg	720		
110	Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp			
111	225 230 235 240			
113	tgt ttc cag agc gtg ttg acc gtg cgc agt ctg aag gac aga gat aac	768		
114	Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn			
115	245 250 255			
117	caa ttc tat cgc tct cag tat aag aag gag gcc att ggc ctc gcc ctg	816		
118	Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu			
119	260 265 270			
122	cat tgg aca ttg aag gcc ctg ttc cac tta ttc ttt atg ccc agc atc	864		
123	His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile			
124	275 280 285			
126	ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc	912		
127	Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe			
128	290 295 300			

RAW SEQUENCE LISTING

DATE: 09/05/2006

PATENT APPLICATION: US/10/590,457

TIME: 15:11:40

Input Set : E:\Sequence Listing-13987-00020-US.txt

Output Set: N:\CRF4\09052006\J590457.raw

```

130 ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc      960
131 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
132 305                               310                               315                               320
134 ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat      1008
135 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
136                               325                               330                               335
138 gag acc atg aac att cgg cga ggg att atc aca gap tgg ttt ttc gga      1056
139 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
140                               340                               345                               350
142 ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc      1104
143 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
144                               355                               360                               365
146 cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag      1152
147 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
148                               370                               375                               380
150 cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc      1200
151 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
152 385                               390                               395                               400
154 cgg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc      1248
156 Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
157                               405                               410                               415
159 gcg ggg aag gct cta taa      1266
160 Ala Gly Lys Ala Leu
161                               420
164 <210> SEQ ID NO: 2
166 <211> LENGTH: 421
168 <212> TYPE: PRT
170 <213> ORGANISM: Euglena gracilis
174 <400> SEQUENCE: 2
176 Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
177 1                               5                               10                               15
180 Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
181                               20                               25                               30
184 Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
185                               35                               40                               45
188 His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
189                               50                               55                               60
192 Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
193 65                               70                               75                               80
196 Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
197                               85                               90                               95
200 Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
201                               100                              105                              110
204 Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
205                               115                              120                              125
208 Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
209                               130                              135                              140
212 His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
213 145                               150                              155                              160

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/590,457

DATE: 09/05/2006

TIME: 15:11:46

Input Set : E:\Sequence Listing-13987-00020-US.txt

Output Set: E:\CRP4\09052006\J590457.raw

```

216 Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
217      165      170      175
220 Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
221      180      185      190
224 Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
225      195      200      205
228 Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
229      210      215      220
232 Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
233      225      230      235      240
236 Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
237      245      250      255
240 Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
241      260      265      270
244 His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
245      275      280      285
248 Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
249      290      295      300
252 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
253      305      310      315      320
256 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
257      325      330      335
260 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
261      340      345      350
264 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
265      355      360      365
268 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
269      370      375      380
272 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
273      385      390      395      400
276 Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
277      405      410      415
280 Ala Gly Lys Ala Leu
281      420

```

284 <210> SEQ ID NO: 3

286 <211> LENGTH: 777

288 <212> TYPE: DNA

290 <213> ORGANISM: Isochrysis galbana

294 <220> FEATURE:

296 <221> NAME/KEY: CDS

298 <222> LOCATION: (1)..(777)

300 <223> OTHER INFORMATION: Delta-9 elongase

304 <400> SEQUENCE: 3

305 atg gcc ctc gca aac gac gcg gga gag cgc atc tgg gcg gct gtg acc 48

306 Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr

307 1 5 10 15

309 gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta otc aaa ccg 96

310 Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro

311 20 25 30

RAW SEQUENCE LISTING

DATE: 09/05/2006

PATENT APPLICATION: US/10/590,457

TIME: 15:11:48

Input Set : E:\Sequence Listing-13987-00020-US.txt

Output Set: H:\CRF4\09052006\J590457.raw

```

314 ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg 144
315 Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
316 35 40 45
318 acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg 192
319 Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
320 50 55 60
322 agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc 240
323 Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
324 65 70 75 80
326 gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag 288
327 Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
328 85 90 95
330 tgc ccg tcc ccg gtt tgg gac tgg aag ctc ttc aca tgg acc gcc aag 336
331 Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
332 100 105 110
334 gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg ggc tgg ctg 384
335 Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
336 115 120 125
338 agg gtc tcc ttt ctc cag gcc ttc cac cac ttc agc ggc ccg tgg gat 432
339 Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
340 130 135 140
342 gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg 480
343 Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
344 145 150 155 160
347 ttc ttc aac tgg ttc att cac acc atc atg tac acc tac tac ggc ctc 528
348 Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
349 165 170 175
351 acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg 576
352 Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met
353 180 185 190
355 cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc 624
356 Gln Ile Cys Gln Phe Val Gly Phe Leu Leu Val Trp Asp Tyr Ile
357 195 200 205
359 aac gtc ccc tgc ttc aac tgg gac aaa ggg aag ttg ttc agc tgg gct 672
360 Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
361 210 215 220
363 ttc aac tat gca tac gtc ggc tgg gtc ttc ttg ctc ttc tgc cac ttc 720
364 Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
365 225 230 235 240
367 ttc tac cag gac aac ttg gca acg aag aaa tgg gcc aag gcg ggc aag 768
368 Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys
369 245 250 255
371 cag ctc tag 777
372 Gln Leu
376 <210> SEQ ID NO: 4
378 <211> LENGTH: 256
380 <212> TYPE: PRT
382 <213> ORGANISM: Isochrysis galbana
386 <400> SEQUENCE: 4

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7570,437

pg-6

<210> SEQ ID NO 115

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Consensus

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (1)..(13)

<223> OTHER INFORMATION: Xaa in the sequence at positions 2, 3, 4, 6, 7, 8 and 9 has the

meaning given in Table A.

<400> SEQUENCE: 115

Asn Xaa Xaa Xaa His Xaa Xaa Met Tyr Xaa Tyr Tyr Xaa
1 10

Invalid Response. 2137 Responses
Can be either Artificial, Unknown
or genus species. See Item 10
on Error Summary sheet.

Insufficient Explanation.
Pls Explain 'Xaa' Specifically.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/590,457**DATE: 09/05/2006**
TIME: 15:11:49**Input Set : E:\Sequence Listing-13987-00020-US.txt**
Output Set: N:\CRF4\09052006\J590457.raw**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:115; Xaa Pos. 2,3,4,6,7,10,13

Seq#:116; Xaa Pos. 3,4,5,6

Seq#:139; Xaa Pos. 3,4

Seq#:140; Xaa Pos. 2,3,5,6

Seq#:141; Xaa Pos. 3

Seq#:142; Xaa Pos. 5,6

Seq#:185; N Pos. 3,18

Seq#:186; N Pos. 3,9,12,15,21

Invalid <213> Responses:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:121,122,123,124,125,126,127,128,129,130,143,144,145,146,147,148,149,150,151,152,153,154,155,156,157,158,159,160,161,162,163,164,165,166,167,168,169,170,171,172,173,174,175,176,177,178,179,180,181,182,185,186,187,188

Seq#:189,190,191,192,203,204,205,206,207,208,209,210,211,212,213,214,215,216

Seq#:217,218,219,220,221,222,223,224,225,226,227,228,229,230,231,232,233,234

Seq#:235,236,237,238,239,240,241,242,243,244,245,246,247,248,249,250,251,252

Seq#:253,254,255

VERIFICATION SUMMARY

DATE: 09/05/2006

PATENT APPLICATION: US/10/590,457

TIME: 15:11:49

Input Set : E:\Sequence Listing-13987-00020-US.txt

Output Set: N:\CRF4\09052006\J590457.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115 after pos.:0
L:13254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116 after pos.:0
L:14471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:139 after pos.:0
L:14498 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:140 after pos.:0
L:14525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:141 after pos.:0
L:14552 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:142 after pos.:0
L:15228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:185 after pos.:0
L:15246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:186 after pos.:0